ξ NCBI

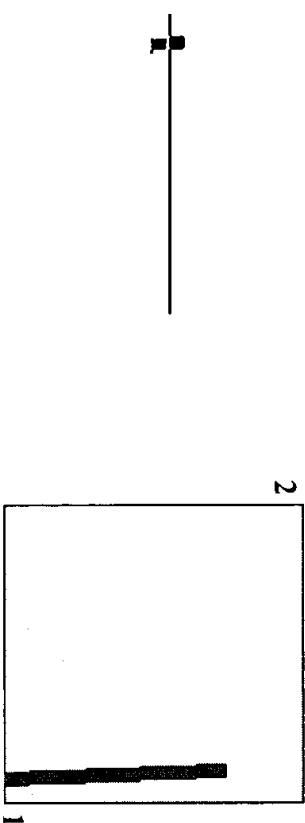| PubMed	Entrez	BLAST	OMIM	Taxonomy	Structure

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: ⌐1   Mismatch: ⌐2   gap open: ⌐5   gap extension: ⌐2

x_dropoff: ⌐50   expect: ⌐10.00   wordsize: ⌐11   Filter ☑   Align

Sequence 1 lcl|seq_1 **Length 9721** (1 .. 9721)
Sequence 2 lcl|seq_2 **Length 415** (1 .. 415)

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence

NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

```
Score =  569 bits (296), Expect = e-158
Identities = 306/309 (99%), Gaps = 1/309 (0%)
Strand = Plus / Minus

Query: 8633  taagaaaccctctgtcattcgtctcccacattctgatgagcaaccgcttccctattattt  8692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct: 308   taagaaaccctctgtcattcgctcccacattctgatgagcaaccgcttccctattattt  249
```

Exhibit B

Blast Result

```
Query: 8693  atttatttgtttgtttgattcattggtctaattttattcaaaggggggcaagaagta  8752
             ||||||||||||||||||||| ||||||||||||||||||||| |||  ||||||||||
Sbjct: 248   atttatttgtttgtttt-attcattggtctaattttattcaaaggggggcaagaagta  190

Query: 8753  gcagtgtctgtaaaagagagcctagtttttaatagctatggaatcaattcaattggactgg  8812
             ||||||||||||||||||| |||||||||||||||||||||||||| |||||||||| ||||
Sbjct: 189   gcagtgtctgtaaaagagagcctagtttttaatagctatggaatcaattcaatttggactgg  130

Query: 8813  tgtgtctctcttataagtcctttaattaacactgaaaatataagctcagatatt  8872
             |||||||||||||||||||| |||||||||||||| |||||||||| |||||||
Sbjct: 129   tgtgtctctcttaaatcaagtccttttaattaacactgnaaatataagctcagatattt  70

Query: 8873  taaatggaatatttatataatgagcaaaatatgatactgttcaatggttctgaaataaact  8932
             |||||||||||||| |||||||||||||||||||| ||||||||||||||||||||||||
Sbjct: 69   taaatggaatatttatataatgagcaaaatatcatactgttcaatggttctgaaataaact  10

Query: 8933  tcactgaag 8941
             |||||||||
Sbjct: 9    tcactgaag 1
```

Lambda   K   H
  1.33   0.621   1.12

Gapped
Lambda   K   H
  1.33   0.621   1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 8
Number of Sequences: 0
Number of extensions: 8
Number of successful extensions: 4
Number of sequences better than 10.0: 1
length of query: 9721
length of database: 7,612,945,758
effective HSP length: 27
effective length of query: 9694
effective length of database: 7,612,945,731
effective search space: 73798959916314

CPU time: 0.19 user secs. 0.04 sys. secs 0.23 total secs.

```
effective search space used: 737989591631\4
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 22 (43.0 bits)
```